

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Meissner, Paul S.  
Coleman, Timothy A.
- (ii) TITLE OF INVENTION: Human CRIPTIN Growth Factor
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Human Genome Sciences, Inc.
  - (B) STREET: 9410 Key West Avenue
  - (C) CITY: Rockville
  - (D) STATE: MD
  - (E) COUNTRY: USA
  - (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 09/393,023
  - (B) FILING DATE: 09-SEP-1999
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/471,371
  - (B) FILING DATE: 06-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Marks, Michelle S.
  - (B) REGISTRATION NUMBER: 41,971
  - (C) REFERENCE/DOCKET NUMBER: PF200D1
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 301-309-8504
  - (B) TELEFAX: 301-309-8439

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 672 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..672

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	ACC	TGG	AGG	CAC	CAT	GTC	AGG	CTT	CTG	TTT	ACG	GTC	AGT	TTG	GCA	48
Met	Thr	Trp	Arg	His	His	Val	Arg	Leu	Leu	Phe	Thr	Val	Ser	Leu	Ala	
1				5					10					15		
TTA	CAG	ATC	ATC	AAT	TTG	GGA	AAC	AGC	TAT	CAA	AGA	GAG	AAA	CAT	AAC	96
Leu	Gln	Ile	Ile	Asn	Leu	Gly	Asn	Ser	Tyr	Gln	Arg	Glu	Lys	His	Asn	
			20					25					30			
GGC	GGT	AGA	GGG	GAA	GTC	ACC	AAG	GTT	GCC	ACT	CAG	AAG	CAC	CGA	CAG	144
Gly	Gly	Arg	Gly	Glu	Val	Thr	Lys	Val	Ala	Thr	Gln	Lys	His	Arg	Gln	
		35					40					45				
TCA	CCG	CTT	AAC	TGG	ACC	TCC	AGT	CAT	TTC	GGA	GAG	GTG	ACT	GGG	AGC	192
Ser	Pro	Leu	Asn	Trp	Thr	Ser	Ser	His	Phe	Gly	Glu	Val	Thr	Gly	Ser	
	50					55					60					
GCC	GAG	GGC	TGG	GGG	CCG	GAG	GAG	CCG	CTC	CCC	TAC	TCC	CGG	GCT	TTC	240
Ala	Glu	Gly	Trp	Gly	Pro	Glu	Glu	Pro	Leu	Pro	Tyr	Ser	Arg	Ala	Phe	
65					70					75					80	
GGA	GAG	GGT	GCG	TCC	GCG	CGG	CCG	CGC	TGC	TGC	AGG	AAC	GGC	GGT	ACC	288
Gly	Glu	Gly	Ala	Ser	Ala	Arg	Pro	Arg	Cys	Cys	Arg	Asn	Gly	Gly	Thr	
				85					90					95		
TGC	GTG	CTG	GGC	AGC	TTC	TGC	GTG	TGC	CCG	GCC	CAC	TTC	ACC	GGC	CGC	336
Cys	Val	Leu	Gly	Ser	Phe	Cys	Val	Cys	Pro	Ala	His	Phe	Thr	Gly	Arg	
			100					105					110			
TAC	TGC	GAG	CAT	GAC	CAG	AGG	CGC	AGT	GAA	TGC	GGC	GCC	CTG	GAG	CAC	384
Tyr	Cys	Glu	His	Asp	Gln	Arg	Arg	Ser	Glu	Cys	Gly	Ala	Leu	Glu	His	
		115					120					125				
GGA	GCC	TGG	ACC	CTC	CGC	GCC	TGC	CAC	CTC	TGC	AGG	TGC	ATC	TTC	GGG	432
Gly	Ala	Trp	Thr	Leu	Arg	Ala	Cys	His	Leu	Cys	Arg	Cys	Ile	Phe	Gly	
	130					135					140					
GCC	CTG	CAC	TGC	CTC	CCC	CTC	CAG	ACG	CCT	GAC	CGC	TGT	GAC	CCG	AAA	480
Ala	Leu	His	Cys	Leu	Pro	Leu	Gln	Thr	Pro	Asp	Arg	Cys	Asp	Pro	Lys	
145					150					155					160	
GAC	TTC	CTG	GCC	TCC	CAC	GCT	CAC	GGG	CCG	AGC	GCC	GGG	GGC	GCG	CCC	528
Asp	Phe	Leu	Ala	Ser	His	Ala	His	Gly	Pro	Ser	Ala	Gly	Gly	Ala	Pro	
				165					170					175		
AGC	CTG	CTA	CTC	TTG	CTG	CCC	TGC	GCA	CTC	CTG	CAC	CGC	CTC	CTG	CGC	576
Ser	Leu	Leu	Leu	Leu	Leu	Pro	Cys	Ala	Leu	Leu	His	Arg	Leu	Leu	Arg	
			180					185					190			
CCG	GAT	GCG	CCC	GCG	CAC	CCT	CGG	TCC	CTG	GTC	CCT	TCC	GTC	CTC	CAG	624
Pro	Asp	Ala	Pro	Ala	His	Pro	Arg	Ser	Leu	Val	Pro	Ser	Val	Leu	Gln	
		195					200					205				
CGG	GAG	CGG	CGC	CCC	TGC	GGA	AGG	CCG	GGA	CTT	GGG	CAT	CGC	CTT	TAA	672
Arg	Glu	Arg	Arg	Pro	Cys	Gly	Arg	Pro	Gly	Leu	Gly	His	Arg	Leu	*	
	210					215					220					

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Thr	Trp	Arg	His	His	Val	Arg	Leu	Leu	Phe	Thr	Val	Ser	Leu	Ala	
1				5					10					15		
Leu	Gln	Ile	Ile	Asn	Leu	Gly	Asn	Ser	Tyr	Gln	Arg	Glu	Lys	His	Asn	
			20				25						30			
Gly	Gly	Arg	Gly	Glu	Val	Thr	Lys	Val	Ala	Thr	Gln	Lys	His	Arg	Gln	
		35					40					45				
Ser	Pro	Leu	Asn	Trp	Thr	Ser	Ser	His	Phe	Gly	Glu	Val	Thr	Gly	Ser	
	50					55					60					
Ala	Glu	Gly	Trp	Gly	Pro	Glu	Glu	Pro	Leu	Pro	Tyr	Ser	Arg	Ala	Phe	
65					70					75					80	
Gly	Glu	Gly	Ala	Ser	Ala	Arg	Pro	Arg	Cys	Cys	Arg	Asn	Gly	Gly	Thr	
				85					90					95		
Cys	Val	Leu	Gly	Ser	Phe	Cys	Val	Cys	Pro	Ala	His	Phe	Thr	Gly	Arg	
		100						105					110			
Tyr	Cys	Glu	His	Asp	Gln	Arg	Arg	Ser	Glu	Cys	Gly	Ala	Leu	Glu	His	
		115					120					125				
Gly	Ala	Trp	Thr	Leu	Arg	Ala	Cys	His	Leu	Cys	Arg	Cys	Ile	Phe	Gly	
	130					135					140					
Ala	Leu	His	Cys	Leu	Pro	Leu	Gln	Thr	Pro	Asp	Arg	Cys	Asp	Pro	Lys	
145					150					155					160	
Asp	Phe	Leu	Ala	Ser	His	Ala	His	Gly	Pro	Ser	Ala	Gly	Gly	Ala	Pro	
				165					170					175		
Ser	Leu	Leu	Leu	Leu	Leu	Pro	Cys	Ala	Leu	Leu	His	Arg	Leu	Leu	Arg	
		180					185						190			
Pro	Asp	Ala	Pro	Ala	His	Pro	Arg	Ser	Leu	Val	Pro	Ser	Val	Leu	Gln	
	195						200					205				
Arg	Glu	Arg	Arg	Pro	Cys	Gly	Arg	Pro	Gly	Leu	Gly	His	Arg	Leu	*	
	210					215					220					

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACTCTTGGAT CCAATTTGGG AAACAGCTAT CAAAGA 36

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TACAACCTCTA GACTATTATT TACAACATAG AAAATTAAAG GC 42

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACTCTTGGAT CCGCCATCAT GACCTGGAGG CACCAT 36

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TACAACTCTA GACTATTATT TACAACATAG AAAATTAAAG GC

42

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 174 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	His	Ala	Ala	Ile	Ser	Lys	Val	Phe	Glu	Leu	Gly	Leu	Val	Ala	Gly	
1				5					10					15		
Leu	Gly	His	Gln	Glu	Phe	Ala	Arg	Pro	Ser	Arg	Gly	Tyr	Leu	Ala	Phe	
			20					25					30			
Arg	Asp	Asp	Ser	Ile	Trp	Pro	Gln	Glu	Glu	Pro	Ala	Ile	Arg	Pro	Arg	
		35					40					45				
Ser	Ser	Gln	Arg	Val	Pro	Pro	Met	Gly	Ile	Gln	His	Ser	Lys	Glu	Leu	
		50				55					60					
Asn	Arg	Thr	Cys	Cys	Leu	Asn	Gly	Gly	Thr	Cys	Met	Leu	Gly	Ser	Phe	
65					70					75					80	
Cys	Ala	Cys	Pro	Pro	Ser	Phe	Tyr	Gly	Arg	Asn	Cys	Glu	His	Asp	Val	
				85					90					95		
Arg	Lys	Glu	Asn	Cys	Gly	Ser	Val	Pro	His	Asp	Thr	Trp	Leu	Pro	Lys	
			100					105					110			
Lys	Cys	Ser	Leu	Cys	Lys	Cys	Trp	His	Gly	Gln	Leu	Arg	Cys	Phe	Pro	
		115					120					125				
Gln	Ala	Phe	Leu	Pro	Gly	Cys	Asp	Gly	Leu	Val	Met	Asp	Glu	His	Leu	
		130				135					140					
Val	Ala	Ser	Arg	Thr	Pro	Glu	Leu	Pro	Pro	Ser	Ala	Arg	Thr	Thr	Thr	
145					150					155					160	
Phe	Leu	Met	Val	Gly	Ile	Cys	Leu	Ser	Ile	Gln	Ser	Tyr	Tyr			
				165					170							